

[Sequence Listing]

SEQ ID No: 1

Length of Sequence: 1874

5

Type of Sequence: Nucleic Acid

Topology: Linear

Strandness: Double strands

Kinds of Sequence: cDNA to mRNA

Origin

10

Orgnism Name: Tobacco (*Nicotiana tabacum*)

Strain name: Xanthi NC

Character of Sequence

Sign designating character: CDS

Position that locates: 26..1672

15

Way of determining character: P

AGCGCGGTCT ACAAGTCAGG CAGTC ATG ACA ACA ACT CCC ATC GCC AAT CAT 52

Met Thr Thr Thr Pro Ile Ala Asn His

20

1

5

CCT AAT ATT TTC ACT CAC CAG TCG TCG TCA TCG CCA TTG GCA TTC TTA 100

Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu

10

15

20

25

25

AAC CGT ACG AGT TTC ATC CCT TTC TCT TCA ATC TCC AAG CGC AAT AGT 148

Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser

30

35

40

	GTC AAT TGC AAT GGC TGG AGA ACA CGA TGC TCC GTT GCC AAA GAT TAC	196
	Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr	
	45 50 55	
5	ACA GTT CCT TCC TCA GCG GTC GAC GGC GGA CCC GCC GCG GAG CTG GAC	244
	Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp	
	60 65 70	
	TGT GTT ATA GTT GGA GCA GGA ATT AGT GGC CTC TGC ATT GCG CAG GTG	292
10	Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val	
	75 80 85	
	ATG TCC GCT AAT TAC CCC AAT TTG ATG GTA ACC GAG GCG AGA GAT CGT	340
	Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg	
15	90 95 100 105	
	GCC GGT GGC AAC ATA ACG ACT GTG GAA AGA GAC GGC TAT TTG TGG GAA	388
	Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu	
	110 115 120	
20	GAA GGT CCC AAC AGT TTC CAG CCG TCC GAT CCT ATG TTG ACT ATG GCA	436
	Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala	
	125 130 135	
25	GTA GAT TGT GGA TTG AAG GAT GAT TTG GTG TTG GGA GAT CCT AAT GCG	484
	Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala	
	140 145 150	
	CCC CGT TTC GTT TTG TGG AAG GGT AAA TTA AGG CCC GTC CCC TCA AAA	532

Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys

155

160

165

CTC ACT GAT CTT CCC TTT TTT GAT TTG ATG AGC ATT CCT GGC AAG TTG 580

5 Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu

170

175

180

185

AGA GCT GGT TTT GGT GCC ATT GGC CTC CGC CCT TCA CCT CCA GGT CAT 628

Arg Ala Gly Phe Gly Ala Ile Gly Leu Arg Pro Ser Pro Pro Gly His

10

190

195

200

GAG GAA TCA GTT GAG CAG TTC GTG CGT CGT AAT CTT GGT GGC GAA GTC 676

Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val

205

210

215

15

TTT GAA CGC TTG ATA GAA CCA TTT TGT TCT GGT GTT TAT GCT GGT GAT 724

Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp

220

225

230

20 CCC TCA AAA CTG AGT ATG AAA GCA GCA TTT GGG AAA GTT TGG AAG TTG 772

Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu

235

240

245

GAA GAA ACT GGT GGT AGC ATT ATT GGA GGA ACC TTT AAA GCA ATA AAG 820

25 Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys

250

255

260

265

GAG AGA TCC AGT ACA CCT AAA GCG CCC CGC GAT CCG CGT TTA CCT AAA 868

Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys

	270	275	280	
	CCA AAA GGA CAG ACA GTT GGA TCA TTC AGG AAG GGT CTC AGA ATG CTG	916		
	Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu			
	285	290	295	
5	CCG GAT GCA ATC AGT GCA AGA TTG GGA AGC AAA TTA AAA CTA TCA TGG	964		
	Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp			
	300	305	310	
10	AAG CTT TCT AGC ATT ACT AAG TCA GAA AAA GGA GGA TAT CAC TTG ACA	1012		
	Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr			
	315	320	325	
	TAC GAG ACA CCA GAA GGA GTA GTT TCT CTT CAA AGT CGA AGC ATT GTC	1060		
15	Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val			
	330	335	340	345
	ATG ACT GTG CCA TCC TAT GTA GCA AGC AAC ATA TTA CGT CCT CTT TCG	1108		
	Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser			
20	350	355	360	
	GTT GCC GCA GCA GAT GCA CTT TCA AAT TTC TAC TAT CCC CCA GTT GGA	1156		
	Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly			
	365	370	375	
25	GCA GTC ACA ATT TCA TAT CCT CAA GAA GCT ATT CGT GAT GAG CGT CTG	1204		
	Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu			
	380	385	390	

	GTT GAT GGT GAA CTA AAG GGA TTT GGG CAG TTG CAT CCA CGT ACA CAG	1252
	Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln	
	395 400 405	
5	GGA GTG GAA ACA CTA GGA ACG ATA TAT AGT TCA TCA CTC TTC CCT AAC	1300
	Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn	
	410 415 420 425	
	CGT GCC CCA AAA GGT CGG GTG CTA CTC TTG AAC TAC ATT GGA GGA GCA	1348
10	Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala	
	430 435 440	
	AAA AAT CCT GAA ATT TTG TCT AAG ACG GAG AGC CAA CTT GTG GAA GTA	1396
	Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val	
15	445 450 455	
	GTT GAT CGT GAC CTC AGA AAA ATG CTT ATA AAA CCC AAA GCT CAA GAT	1444
	Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp	
	460 465 470	
20	CCT CTT GTT GTG GGT GTG CGA GTA TGG CCA CAA GCT ATC CCA CAG TTT	1492
	Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe	
	475 480 485	
25	TTG GTT GGT CAT CTG GAT ACG CTA AGT ACT GCA AAA GCT GCT ATG AAT	1540
	Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn	
	490 495 500 505	
	GAT AAT GGG CTT GAA GGG CTG TTT CTT GGG GGT AAT TAT GTG TCA GGT	1588

Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly

510

515

520

GTA GCA TTG GGG AGG TGT GTT GAA GGT GCT TAT GAA GTT GCA TCC GAG 1636

5 Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu

525

530

535

GTA ACA GGA TTT CTG TCT CGG TAT GCA TAC AAA TGAAACCTGT GTTGGGGGTA 1689

Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys

10

540

545

GTCCAAACCT TGTTAGTAGT ACGATCATGC CTTGGGAAAA TTGGCATGTG CCTAAAGTT 1749

TTGCTCATTAGAGTTATTTT AGCCTTGGTA AATGATTGT ACTTGATATC AGTCGTTTTTC 1809

TTTGAGATAA AATGTTCTCTG TTCAGGAAAT ATAATGTATA TCAATTTTAA AAAAAAAAAA 1869

AAAAA 1874

15

SEQ ID No.: 2

Length of Sequence: 548

Type of Sequence: Amino acid

Topology: Linear

5 Kind of Sequence: Protein

Origin:

Organism Name: Tobacco (*Nicotiana tabacum*)

Strain name: SR1

10

Met Thr Thr Thr Pro Ile Ala Asn His Pro Asn Ile Phe Thr His Gln  
1 5 10 15

Ser Ser Ser Ser Pro Leu Ala Phe Leu Asn Arg Thr Ser Phe Ile Pro  
15 20 25 30

Phe Ser Ser Ile Ser Lys Arg Asn Ser Val Asn Cys Asn Gly Trp Arg  
35 40 45

20 Thr Arg Cys Ser Val Ala Lys Asp Tyr Thr Val Pro Ser Ser Ala Val  
50 55 60

Asp Gly Gly Pro Ala Ala Glu Leu Asp Cys Val Ile Val Gly Ala Gly  
65 70 75 80

25

Ile Ser Gly Leu Cys Ile Ala Gln Val Met Ser Ala Asn Tyr Pro Asn  
85 90 95

Leu Met Val Thr Glu Ala Arg Asp Arg Ala Gly Gly Asn Ile Thr Thr

	100	105	110
	Val Glu Arg Asp Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln		
	115	120	125
5	Pro Ser Asp Pro Met Leu Thr Met Ala Val Asp Cys Gly Leu Lys Asp		
	130	135	140
	Asp Leu Val Leu Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Lys		
10	145	150	155
	Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr Asp Leu Pro Phe Phe		
	165	170	175
15	Asp Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Phe Gly Ala Ile		
	180	185	190
	Gly Leu Arg Pro Ser Pro Pro Gly His Glu Glu Ser Val Glu Gln Phe		
	195	200	205
20	Val Arg Arg Asn Leu Gly Gly Glu Val Phe Glu Arg Leu Ile Glu Pro		
	210	215	220
	Phe Cys Ser Gly Val Tyr Val Gly Asp Pro Ser Lys Leu Ser Met Lys		
25	225	230	235
	Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Glu Thr Gly Gly Ser Ile		
	245	250	255

Ile Gly Gly Thr Phe Lys Ala Ile Lys Glu Arg Ser Ser Thr Pro Lys

260

265

270

Ala Pro Arg Asp Pro Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly

5

275

280

285

Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Asp Ala Ile Ser Ala Arg

290

295

300

10 Leu Gly Ser Lys Leu Lys Leu Ser Trp Lys Leu Ser Ser Ile Thr Lys

305

310

315

320

Ser Glu Lys Gly Gly Tyr His Leu Thr Tyr Glu Thr Pro Glu Gly Val

325

330

335

15

Val Ser Leu Gln Ser Arg Ser Ile Val Met Thr Val Pro Ser Tyr Val

340

345

350

Ala Ser Asn Ile Leu Arg Pro Leu Ser Val Ala Ala Ala Asp Ala Leu

20

355

360

365

Ser Asn Phe Tyr Tyr Pro Pro Val Gly Ala Val Thr Ile Ser Tyr Pro

370

375

380

25 Gln Glu Ala Ile Arg Asp Glu Arg Leu Val Asp Gly Glu Leu Lys Gly

385

390

395

400

Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val Glu Thr Leu Gly Thr

405

410

415

Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Lys Gly Arg Val  
 420 425 430

5 Leu Leu Leu Asn Tyr Ile Gly Gly Ala Lys Asn Pro Glu Ile Leu Ser  
 435 440 445

Lys Thr Glu Ser Gln Leu Val Glu Val Val Asp Arg Asp Leu Arg Lys  
 450 455 460

10

Met Leu Ile Lys Pro Lys Ala Gln Asp Pro Leu Val Val Gly Val Arg  
 465 470 475 480

15 Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Thr  
 485 490 495

Leu Ser Thr Ala Lys Ala Ala Met Asn Asp Asn Gly Leu Glu Gly Leu  
 500 505 510

20 Phe Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val  
 515 520 525

Glu Gly Ala Tyr Glu Val Ala Ser Glu Val Thr Gly Phe Leu Ser Arg  
 530 535 540

25

Tyr Ala Tyr Lys  
 545

SEQ ID No.: 3

Length of Sequence: 1874

type of Sequence: Nucleic acid

Topology: Linear

5

Strandness: Double strands

Kind of Sequence: cDNA to mRNA

Origin

Organism Name: tobacco (*Nicotiana tabacum*)

Strain Name: SR1

10

Character of Sequence

Signal designating Character: CDS

Location: 26..1672

way for determining Character: P

15

AGCGCGGTCT ACAAGTCAGG CAGTC ATG ACA ACA ACT CCC ATC GCC AAT CAT 52

Met Thr Thr Thr Pro Ile Ala Asn His

1

5

20

CCT AAT ATT TTC ACT CAC CAG TCG TCG TCA TCG CCA TTG GCA TTC TTA 100

Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu

10

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20

25

25 AAC CGT ACG AGT TTC ATC CCT TTC TCT TCA ATC TCC AAG CGC AAT AGT 148

Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser

30

35

40

GTC AAT TGC AAT GGC TGG AGA ACA CGA TGC TCC GTT GCC AAA GAT TAC 196

	Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr	
	45 50 55	
	ACA GTT CCT TCC TCA GCG GTC GAC GGC GGA CCC GCC GCG GAG CTG GAC	244
5	Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp	
	60 65 70	
	TGT GTT ATA GTT GGA GCA GGA ATT AGT GGC CTC TGC ATT GCG CAG GTG	292
	Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val	
10	75 80 85	
	ATG TCC GCT AAT TAC CCC AAT TTG ATG GTA ACC GAG GCG AGA GAT CGT	340
	Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg	
	90 95 100 105	
15		
	GCC GGT GGC AAC ATA ACG ACT GTG GAA AGA GAC GGC TAT TTG TGG GAA	388
	Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu	
	110 115 120	
20	GAA GGT CCC AAC AGT TTC CAG CCG TCC GAT CCT ATG TTG ACT ATG GCA	436
	Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala	
	125 130 135	
	GTA GAT TGT GGA TTG AAG GAT GAT TTG GTG TTG GGA GAT CCT AAT GCG	484
25	Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala	
	140 145 150	
	CCC CGT TTC GTT TTG TGG AAG GGT AAA TTA AGG CCC GTC CCC TCA AAA	532
	Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys	

	155	160	165	
	CTC ACT GAT CTT CCC TTT TTT GAT TTG ATG AGC ATT CCT GGC AAG TTG			580
	Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu			
5	170	175	180	185
	AGA GCT GGT TTT GGT GCC ATT GGC CTC CGC CCT TCA CCT CCA GGT CAT			628
	Arg Ala Gly Phe Gly Ala Ile Gly Leu Arg Pro Ser Pro Pro Gly His			
	190	195	200	
10	GAG GAA TCA GTT GAG CAG TTC GTG CGT CGT AAT CTT GGT GGC GAA GTC			676
	Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val			
	205	210	215	
15	TTT GAA CGC TTG ATA GAA CCA TTT TGT TCT GGT GTT TAT GTT GGT GAT			724
	Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Val Gly Asp			
	220	225	230	
	CCC TCA AAA CTG AGT ATG AAA GCA GCA TTT GGG AAA GTT TGG AAG TTG			772
20	Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu			
	235	240	245	
	GAA GAA ACT GGT GGT AGC ATT ATT GGA GGA ACC TTT AAA GCA ATA AAG			820
	Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys			
25	250	255	260	265
	GAG AGA TCC AGT ACA CCT AAA GCG CCC CGC GAT CCG CGT TTA CCT AAA			868
	Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys			
	270	275	280	

CCA AAA GGA CAG ACA GTT GGA TCA TTC AGG AAG GGT CTC AGA ATG CTG 916

Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu

285

290

295

5 CCG GAT GCA ATC AGT GCA AGA TTG GGA AGC AAA TTA AAA CTA TCA TGG 964

Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp

300

305

310

AAG CTT TCT AGC ATT ACT AAG TCA GAA AAA GGA GGA TAT CAC TTG ACA 1012

10 Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr

315

320

325

TAC GAG ACA CCA GAA GGA GTA GTT TCT CTT CAA AGT CGA AGC ATT GTC 1060

Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val

15 330 335 340 345

ATG ACT GTG CCA TCC TAT GTA GCA AGC AAC ATA TTA CGT CCT CTT TCG 1108

Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser

350

355

360

20

GTT GCC GCA GCA GAT GCA CTT TCA AAT TTC TAC TAT CCC CCA GTT GGA 1156

Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly

365

370

375

25 GCA GTC ACA ATT TCA TAT CCT CAA GAA GCT ATT CGT GAT GAG CGT CTG 1204

Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu

380

385

390

GTT GAT GGT GAA CTA AAG GGA TTT GGG CAG TTG CAT CCA CGT ACA CAG 1252

Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln

395

400

405

GGA GTG GAA ACA CTA GGA ACG ATA TAT AGT TCA TCA CTC TTC CCT AAC 1300

5 Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn

410

415

420

425

CGT GCC CCA AAA GGT CGG GTG CTA CTC TTG AAC TAC ATT GGA GGA GCA 1348

Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala

10

430

435

440

AAA AAT CCT GAA ATT TTG TCT AAG ACG GAG AGC CAA CTT GTG GAA GTA 1396

Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val

445

450

455

15

GTT GAT CGT GAC CTC AGA AAA ATG CTT ATA AAA CCC AAA GCT CAA GAT 1444

Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp

460

465

470

20 CCT CTT GTT GTG GGT GTG CGA GTA TGG CCA CAA GCT ATC CCA CAG TTT 1492

Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe

475

480

485

TTG GTT GGT CAT CTG GAT ACG CTA AGT ACT GCA AAA GCT GCT ATG AAT 1540

25 Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn

490

495

500

505

GAT AAT GGG CTT GAA GGG CTG TTT CTT GGG GGT AAT TAT GTG TCA GGT 1588

Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly

510

515

520

GTA GCA TTG GGG AGG TGT GTT GAA GGT GCT TAT GAA GTT GCA TCC GAG 1636

Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu

5

525

530

535

GTA ACA GGA TTT CTG TCT CGG TAT GCA TAC AAA TGAAACCTGT GTTGGGGGTA 1689

Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys

540

545

10 GTCCAAACCT TGTAGTAGT ACGATCATGC CTTGGGAAAA TTGGCATGTG CCTAAAAAGTT 1749

TTGCTCATTAGAGTTATTTT AGCCTTGCGTA AATGATTTGT ACTTGATATC AGTCGTTTTTC 1809

TTTGAGATAA AATGTTCTCG TTCAGGAAAT ATAATGTATA TCAATTTTAA AAAAAAAAAA 1869

AAAAA 1874

15

SEQ ID No.: 4

Length of Sequence: 23

type of Sequence: Nucleic acid

Strandness: single strand

5

topology: straight

kind of Sequence: other nucleic acid synthetic oligonucleotide

ATTGGTGGCG ACGACTCCTG GAG

10

SEQ ID No.: 5

Length of Sequence: 24

Type of Sequence: Nucleic acid

Strandness: single strand

15

Topology: straight

Kind of Sequence: other nucleic acid synthetic oligonucleotide

CCAGACCAAC TGGTAATGGT AGCG

20

SEQ ID No.: 6

Length of Sequence: 24

Type of Sequence: Nucleic acid

Strandness: single strand

25

topology: straight

Kind of Sequence: other nucleic acid synthetic oligonucleotide

GCGGTCTACA AGTCAGGCAG TCAT

SEQ ID No. : 7

Length of Sequence : 31

Type of Sequence : Nucleic acid

5 Strandness : single strand

Topology : straight

Kind of Sequence : other nucleic acid synthetic oligonucleotide

CATGCCAATT TTCCAAGGC ATGATCGTAC T

10

SEQ ID No. : 8

Length of Sequence : 20

Type of Sequence : Nucleic acid

Strandness : single strand

15

Topology : straight

kind of Sequence : other nucleic acid synthetic oligonucleotide

GGTGTATG TTGGTGATCC

20

## Sequence Listing 9

SEQ ID No.: 9

Length of Sequence: 27

Type of Sequence: Nucleic acid

5 Strandness: single strand

Topology: straight

Kind of Sequence: other nucleic acid synthetic oligonucleotide

CACAGATGGT TAGAGAGGCT TACGCAG

10

## Sequence Listing 10

SEQ ID No.: 10

Length of Sequence: 27

15 Type of Sequence: Nucleic acid

Number of chain: single strand

Topology: straight

kind of Sequence: other nucleic acid synthetic oligonucleotide

20 TCATCGCAAG ACCGGCAACA GGATTCA